REMARKS

Applicants express their appreciation to Examiner Moran for discussing the July 17, 2002 Office Action with their undersigned agents on October 10, 2002. This Amendment follows those discussions.

Applicants propose amended claims 19-21 in response to the Examiner's rejections (see below). Support for these amendments appears in former claims 19-21 and throughout the specification as originally filed. Specifically, the computational evaluation of at least one of a plurality of chemical entities finds support, e.g., at page 17, lines 20-26 and page 20, lines 17-22. The positioning step finds support, e.g., at page 17, lines 12-18; page 20, lines 3-10 and especially page 20, lines 31-33. The selecting step finds support, e.g., at page 20, lines 17-22. Applicants have also amended the form of claims 19-21 for clarity.

Applicants have submitted herewith an Appendix, Marked up claims showing the amendments. In the Appendix, the added portions are underlined and the deleted portions are bracketed.

None of these amendments adds new matter.

The Rejections

35 U.S.C. § 101

Claims 19-24 stand rejected under 35 U.S.C. § 101 as being directed to non-statutory subject matter. In a telephone conference on October 10, 2002 and in her July 17, 2002 Office Action, the Examiner preliminarily agreed with applicants that there is no absolute requirement under section 101 for a transformation of data step or a step performing a physical act outside the computer. However, the Examiner has maintained her

contention that the result recited in applicants' claims is merely an output of mathematical data, and does not indicate whether or how the result is to be applied. The Examiner therefore contends that applicants' result is neither practical nor useful, and is merely an invitation to do further research. In light of the proposed claim amendments, applicants assert that these rejections have been overcome.

Applicants' amended claims 19-21 recite the additional step of "selecting at least one of said plurality if chemical entities." As amended, the methods of claims 19-21 produce a useful, concrete, and tangible result; namely, the selection of at least one chemical entity. Accordingly, applicants assert that the claims are directed to statutory subject matter and are useful under section 101. Applicants therefore request that the Examiner withdraw these rejections.

35 U.S.C. § 103

Claims 19-24 stand rejected under 35 U.S.C. § 103(a) as obvious in view of United States Patent No. 5,705,335 (hereinafter "Hendry"). Specifically, the Examiner has maintained her contention that the structure coordinates in applicants' claims are not given patentable weight. The Examiner contends that the structure coordinates in applicants' claims are nonfunctional descriptive material and are neither a data structure nor a program. The Examiner further contends that the computational means of applicants' claims do not functionally interact with the data. In light of the proposed claim amendments, applicants assert that these rejections have been overcome.

Applicants' amended claims recite the additional step of "positioning a graphical three-dimensional representation of the structure of one of said plurality of chemical entities" within the CnA or CnA/CnB binding pocket defined by CnA or

CnA/CnB structure coordinates. Applicants' amended claims additionally clarify that the computational means "utilize said graphical representation of the structure and said structure coordinates." As amended, applicants' claims more clearly set forth the functional interrelationship between the computational means and the structure coordinates of the CnA-like or CnA/CnB-like molecule or molecular complex. Applicants assert that this functional interrelationship confers patentable weight to the structure coordinates. Accordingly, the structure coordinates distinguish applicants' claims from Hendry. Applicants therefore request that the Examiner withdraw these section 103 rejections.

Conclusion

Applicants request that the Examiner enter the above amendments, consider the foregoing remarks and allow the pending claims to issue. If the Examiner believes that a telephonic interview would be helpful, she is invited to call applicants' agent or attorney at any time.

Respectfully submitted,

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APPENDIX

MARKED UP CLAIMS SHOWING THE AMENDMENTS

19. (Four Times Amended) A method of using a computer for evaluating the ability of [a] at least one of a plurality of chemical [entity] entities to associate with a crystallized molecule or molecular complex comprising a calcineurin A (CnA) binding pocket defined by structure coordinates of CnA amino acids 90, 91, 92, 118, 120, 121, 122, 150, 151, 156, 160, 199, 232, 253, 254, 256, 281, 282, 283, 284, 306, 311, 312, and 317 according to Figure 1, or a homologue of said molecule or molecular complex wherein said homologue comprises a CnA homologue binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å;

wherein said computer comprises a machine-readable data storage medium comprising a data storage material encoded with said structure coordinates defining said binding pocket and wherein said method comprises the steps of:

[a.] a) positioning a graphical three-dimensional representation of the structure of one of said plurality of chemical entities within the CnA binding pocket or the CnA homologue binding pocket;

b) [employing computational means to perform a fitting operation between the chemical entity and the CnA binding pocket or the CnA homologue binding pocket] performing a fitting operation between said graphical representation of the structure of said chemical entity and the CnA binding pocket or the CnA homologue binding pocket by employing computational means which utilize said graphical representation of the structure and said structure coordinates;

[b.] c) analyzing the results of said fitting operation to quantify the association between [the] said chemical entity and the CnA binding pocket or the CnA homologue binding pocket; [and]

[c.] d) outputting said quantified association to a suitable output hardware;

e) optionally repeating steps a) through d) with another of said plurality of chemical entities; and

f) selecting at least one of said plurality of chemical entities that associates with the CnA binding pocket or the CnA homologue binding pocket based on said quantified association of said chemical entity.

20. (Four Times Amended) A method of using a computer for evaluating the ability of [a] at least one of a plurality of chemical [entity] entities to associate with a crystallized molecule or molecular complex comprising a CnA binding pocket defined by structure coordinates of CnA amino acids 90, 91, 92, 118, 120, 121, 122, 150, 151, 156, 160, 199, 281, 282, 283, 306, 311, 232, and 254, according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a CnA homologue binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å;

wherein said computer comprises a machine-readable data storage medium comprising a data storage material encoded with said structure coordinates defining said binding pocket and wherein said method comprises the steps of:

[a.] a) positioning a graphical three-dimensional representation of the structure of one of said plurality of chemical entities within the CnA binding pocket or the CnA homologue binding pocket;

b) [employing computational means to perform a fitting operation between the chemical entity and the CnA binding pocket or the CnA homologue binding pocket] performing a fitting operation between said graphical representation of the structure of said chemical entity and the CnA binding pocket or the CnA homologue binding pocket by employing computational means which utilize said graphical representation of the structure and said structure coordinates;

[b.] c) analyzing the results of said fitting operation to quantify the association between [the] said chemical entity and the CnA binding pocket or the CnA homologue binding pocket; [and]

[c.] d) outputting said quantified association to a suitable output hardware;

e) optionally repeating steps a) through d) with another of said plurality of chemical entities; and

f) selecting at least one of said plurality of chemical entities that associates with the CnA binding pocket or the CnA homologue binding pocket based on said quantified association of said chemical entity.

21. (Four Times Amended) A method of using a computer for evaluating the ability of [a] at least one of a plurality of chemical [entity] entities to associate with a crystallized molecule or molecular complex comprising a CnA/CnB binding pocket defined by structure coordinates of CnA amino acids 122, 124, 159, 160, 310, 312, 313, 314, 339, 341, 343, 344, 345, 347, 351, 352, 353, 354, 355, 356, 359, 360, and 363; and calcineurin B (CnB) amino acids 49, 50, 114, 115, 118, 119, 121, 122, 123, 124, 157, 158, 159, 161, and 162 according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a CnA/CnB homologue binding pocket that has a root mean square deviation from the backbone atoms of said CnA and CnB amino acids of not more than 1.5 Å;

wherein said computer comprises a machine-readable data storage medium comprising a data storage material encoded with said structure coordinates defining said binding pocket and wherein said method comprises the steps of:

[a.] a) positioning a graphical three-dimensional representation of the structure of one of said plurality of chemical entities within the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket;

b) [employing computational means to perform a fitting operation between the chemical entity and the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket] performing a fitting operation between said graphical representation of the structure of said chemical entity and the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket by employing computational means which utilize said graphical representation of the structure and said structure coordinates;

[b.] c) analyzing the results of said fitting operation to quantify the association between [the] said chemical entity and the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket; [and]

[c.] d) outputting said quantified association to a suitable output hardware;

e) optionally repeating steps a) through d) with another of

said plurality of chemical entities; and

f) selecting at least one of said plurality of chemical entities that associates with the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket based on said quantified association of said chemical entity.